Antimicrobial Susceptibility of Clinically Relevant Gram-Positive Anaerobic Cocci Collected over a Three-Year Period in the Netherlands[∇]†

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The susceptibility of 14 species of 115 Gram-positive anaerobic cocci (GPAC) was determined for 14 antibiotics. To assure correct identification, strains were genotypically identified by fluorescence in situ hybridization and sequencing. Susceptibility differences (MIC $_{50}$ and MIC $_{90}$) for penicillin G, clindamycin, tigecycline, levofloxacin, amoxicillin-clavulanic acid, cefoxitin, ertapenem, meropenem, metronidazole, and doxycycline were found for the three clinically most relevant GPAC species: Finegoldia magna, Parvimonas micra, and Peptoniphilus harei.

Gram-positive anaerobic cocci (GPAC) are part of the commensal microbiota and account for about one-third of the anaerobic isolates recovered from clinical materials (14). It is a heterogeneous group, which in the last decade has undergone an extensive taxonomic change. The species Peptostreptococcus micros and Peptostreptococcus magnus were transferred to two new genera, Micromonas and Finegoldia, respectively, with each being the only species present in their respective genus (15). The genus Micromonas has recently been replaced by Parvimonas, with Parvimonas micra (Pa. micra) being the only species present (20). Ezaki et al. (7) divided the remaining peptostreptococci into three phylogenetic groups, Peptoniphilus gen. nov., Anaerococcus gen. nov., and Gallicola gen. nov., with Gallicola barnesae being the only species present in the latter genus. The species left in the genus Peptostreptococcus include Peptostreptococcus anaerobius (Pe. anaerobius) and a recently described new species, *Pe. stomatis* (6). Song et al. (19) described three new species: Peptoniphilus gorbachii (Pt. gorbachii) sp. nov., Pt. olsenii sp. nov., and Anaerococcus murdochii sp. nov. The most commonly found GPAC in clinical material are Finegoldia magna, Pa. micra, Pt. harei (21), and Pe. anaerobius (22). The data on the antimicrobial susceptibility of the different species of GPAC is often based on GPAC in general, even though several authors describe a difference in antimicrobial susceptibility between species (3–5, 11, 12, 18). In these studies, the strains were identified phenotypically. However, for some species it is difficult to obtain a reliable phenotypic identification, e.g., in the past Pt. harei has often been misidentified as Pt. asaccharolyticus (21), probably due to the fact that these two species share the same biochemical characteristics (10).

In the present study, we assessed the susceptibility of 115 isolates of GPAC against 14 different antibiotics. Isolates were genotypically identified by using fluorescence *in situ* hybridization (FISH) (21) or sequencing, thus allowing more accurate insight into the distribution of susceptible and resistant strains within the different species.

MATERIALS AND METHODS

Isolates. Strains were obtained from the diagnostic laboratory of the University Medical Center Groningen and collected in the years 2002 to 2004. All strains were isolated from human clinical samples from a variety of anatomical sites, e.g., from abdominal, head and neck, and soft tissue infections. Strains were stored at -80° C and subcultured on brucella blood agar (BBA) prior to susceptibility testing

Identification. Strains were genotypically identified by using 16S rRNA-based probes (21) and sequencing. Shortly thereafter, bacterial cells were harvested from BBA using a sterile loop and fixed in 1:1 phosphate-buffered saline (8 g of NaCl, 0.2 g of KCl, 1.44 g of Na₂HPO₄, and 0.24 g of KH₂PO₄ per liter) and ethanol 96% (vol/vol). Fixed cells were spotted on slides and, if necessary, permeabilized using proteinase K. Strains were hybridized by using probes directed against F. magna, Pa. micra, Pt. harei, Pe. anaerobius, A. vaginalis, Pt. asaccharolyticus, A. lactolyticus, and Pt. ivorii. The addition of new species to the genera Peptoniphilus and Anaerococcus (19) showed that the probes directed against A. lactolyticus and Pt. harei were also positive, with A. murdochii and Pt. gorbachii, respectively (data not shown). Strains that were negative with the probes or positive with the probes directed against A. lactolyticus and Pt. harei were sequenced. DNA was isolated as described previously (2), and the 16S genes were amplified and sequenced using universal 16S rRNA-specific primers (9). Sequences were compared to those in the GenBank database by performing a BLAST search (National Center of Biotechnology Information) (1).

Susceptibility testing. The antimicrobial susceptibility using penicillin G, amoxicillin-clavulanic acid, cefotetan, cefoxitin, ertapenem, meropenem, levofloxacin, moxifloxacin, clindamycin, metronidazole, linezolid, chloramphenicol, doxycycline, and tigecycline was determined by using Etest (AB Biodisk, Sweden). Suspensions of approximately 2 McFarland standards were made in prereduced brucella broth and applied onto a prereduced BBA. All culture handlings were performed in an anaerobic chamber. Plates with Etest strips were incubated for 48 h at 37°C in an anaerobic chamber before reading the MIC. In each batch a quality control strain *Bacteroides fragilis* ATCC 25285 was included.

A difference in susceptibility was defined as at least a two-dilution-step (with one dilution step being a difference of 2-fold dilutions with a precision of a 0.5 dilution) difference between the MIC's of the different species.

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TABLE 1. MIC values determined from the quality control tests on B. fragilis ATCC 25285

	MIC (mg/liter)					
Antibiotic	MICs (no. of tests)	Expected MIC range ^a				
Penicillin G	12 (2), 16 (7), 24 (1)	8–32				
Amoxicillin-clavulanic acid	0.19 (2), 0.25 (5), 0.38 (3)	0.125-0.5†				
Cefotetan	6 (7), 8 (3)	4-16				
Cefoxitin	4 (1), 6 (7), 8 (2)	4-16				
Ertapenem	0.125 (4), 0.19 (6)	0.064-0.25				
Meropenem	0.094 (2), 0.125 (4), 0.19 (4)	0.064-0.25				
Levofloxacin	1 (1), 1.5 (9)	1*				
Moxifloxacin	0.19 (1), 0.25 (1), 0.38 (6), 0.5 (2)	0.125-0.5				
Clindamycin	1.5 (2), 2 (4), 3 (4)	0.5-2				
Metronidazole	0.25 (4), 0.38 (4), 0.5 (2)	0.25-1				
Linezolid	4 (1), 6 (5), 8 (3), 12 (1)	2-8*				
Chloramphenicol	6 (3), 8 (7)	2-8				
Doxycycline	0.25 (3), 0.38 (5), 0.5 (2)	0.25-0.5*				
Tigecycline	0.25 (2), 0.5 (2), 0.75 (6)	0.125-1*				

^a The expected range is derived from CLSI standards for *B. fragilis* for reference agar dilution testing, except as indicated: *, expected range derived from literature; and †, expected range derived from the manufacturer.

RESULTS

The quality control strain *B. fragilis* ATCC 25285 was tested 10 times with all 14 antibiotics. The obtained MICs are summarized in Table 1.

All results of the clinical isolates are summarized in Table 2 and Table 3. The MIC₅₀ and MIC₉₀ values were only calculated for species for which more than 10 strains were present in the study, i.e., F. magna, Pa. micra, and Pt. harei. Upon comparing the MIC₅₀ and MIC₉₀ values for these three species, F. magna had the highest MIC₅₀ and MIC₉₀ values for penicillin G, amoxicillin-clavulanic acid, clindamycin, and tigecycline. It has the highest MIC₅₀ values for cefotetan, cefoxitin, meropenem, linezolid, and chloramphenicol and the highest MIC₉₀ values for levofloxacin and moxifloxacin. Pa. micra has the lowest MIC₅₀ and MIC₉₀ for levofloxacin, metronidazole, and doxycycline and the lowest MIC90 for amoxicillin-clavulanic acid. Pt. harei has the highest MIC50 for levofloxacin and doxycycline. It has the lowest MIC₅₀ and MIC₉₀ for cefoxitin, ertapenem, and meropenem and the lowest MIC₉₀ for chloramphenicol.

DISCUSSION

Since GPAC can show poor growth, we used a McFarland 2 inoculum. The MICs obtained with the quality control strain *B. fragilis* ATCC 25285 show that most of these values are within the expected range. Comparison between a McFarland standard 1 and 2 inoculum using the quality control strain gave the same MIC value (data not shown). However, 4 of the 10 MIC values obtained for clindamycin were just above the expected range obtained using McFarland standard 2. Since GPAC show poor growth compared to *B. fragilis*, this is not expected to affect our set of data. A practical approach is to use a higher McFarland turbidity as recommended by the manufacturer of Etest.

In the present study strains were identified genotypically,

since phenotypic identification is not always reliable for all species (21). It is difficult to compare our results to other published resistance data, since authors may use different breakpoints. For example, some did use breakpoints advised by the Clinical and Laboratory Standards Institute (CLSI), while others used those advised by EUCAST. Therefore, we have chosen to base a difference in susceptibility on the MIC_{50} and MIC_{90} values, instead of the percentage resistant strains. However, the interpretation of our results using CSLI and EUCAST breakpoints is provided in the supplemental material.

The clinically most important GPAC in our study are *F. magna*, *Pa. micra*, and *Pt. harei*. The latter can be especially difficult to identify phenotypically, since its biochemical features resemble those of *Pt. asaccharolyticus* (10). In the past, *Pt. harei* was probably often misidentified as *Pt. asaccharolyticus*, resulting in limited susceptibility data for this species. Brazier et al. (4) included 44 clinical isolates of *Pt. harei* in a European study; all of them were phenotypically identified. No resistance was reported. In a susceptibility study in England and Wales (5), four clinical isolates of *Pt. harei* were included; all of these were also phenotypically identified. Resistance (MIC > 256) was reported to clindamycin. In our study, the MIC₅₀ and MIC₉₀ values for clindamycin were 0.25 and 1.5, respectively. The latter was the highest MIC found for *Pt. harei*.

Our study is the first to include *Pt. gorbachii* and *A. murdochii*, although the numbers are low. It is worth mentioning that one strain of *A. murdochii* had high MIC values for 4 of the 14 antibiotics: doxycycline, ertapenem, levofloxacin, and penicillin G.

Differences in susceptibility to antibiotics were described for Pe. anaerobius and Pe. stomatis (12). Pe. anaerobius has higher MIC values for amoxicillin, amoxicillin-clavulanic acid, cefoxitin, ertapenem, azithromycin, clindamycin, metronidazole, and moxifloxacin than Pe. stomatis; only the MIC₉₀ of azithromycin and moxifloxacin was not two dilution steps higher. Brazier et al. (5) also suggest that some GPAC species are more resistant to antibiotics than others. For example, Pe. anaerobius had a higher MIC₅₀ for tetracycline but had lower MIC values for erythromycin than did F. magna. Roberts et al. (18) showed that Pe. anaerobius has higher MIC₅₀ and MIC₉₀ values for amoxicillin-clavulanic acid, piperacillin-tazobactam, cefoxitin, cefotetan, and meropenem than did F. magna, Pa. micra, and Pt. asaccharolyticus. Koeth et al. (11) showed that F. magna has a higher MIC₅₀ for clindamycin as Pa. micra and Pe. anaerobius, while Pe. anaerobius has the highest MIC₉₀ for amoxicillin-clavulanic acid.

Metronidazole is often the drug used for empirical treatment of anaerobic infections. However, GPAC strains are described which are resistant to this drug (11, 13, 16). We encountered one strain of *Pa. micra* that was resistant to metronidazole (MIC > 256). Microbiologists should be aware of this possibility. It is remarkable to notice the difference in susceptibility to the different antibiotics between the three most clinically important GPAC: *F. magna*, *Pa. micra*, and *Pt. harei*. Therefore, it is important to identify clinical isolates of GPAC. *F. magna* and *Pa. micra* can be reliably phenotypically identified by using a commercially available enzymatic kit such as Rapid ID 32A (21). However, *Pt. harei* cannot be

TABLE 2. MICs and range for GPAC against 14 antibiotics

Organism (no. of strains) ^a	Antibiotic	MIC (mg/liter)			Organism	Antibiotic	MIC (mg/liter)		
		Range	MIC ₅₀	MIC ₉₀	(no. of strains) ^a	Antibiotic	Range	MIC ₅₀	MIC ₉₀
F. magna (31)	Penicillin G Amoxicillin-clavulanic	0.023-0.38	0.125	0.25		Tigecycline	0.032-0.25		
	Amoxiciiin-ciavuianic	0.094–2	0.25	0.5	Pe. anaerobius (4)	Penicillin G	0.064-2		
	Cefotetan	0.25-4	2	2		Amoxicillin-clavulanic	0.125-4		
	Cefoxitin Ertapenem	0.38-3 0.016-0.19	1 0.064	1.5 0.125		acid Cefotetan	0.5-24		
	Meropenem	0.064-0.25	0.125	0.19		Cefoxitin	0.19–3		
	Levofloxacin	0.094–64	0.75	64		Ertapenem	0.032-0.75		
	Moxifloxacin Clindamycin	0.047-64 0.125->256	0.19 1	6		Meropenem Levofloxacin	0.023-1 0.38-1.5		
	Metronidazole	0.094-1.5	0.38	1		Moxifloxacin	0.19-0.25		
	Linezolid	2–6	3	3		Clindamycin	0.032-1		
	Chloramphenicol Doxycycline	4–16 0.75–24	6 2	8 24		Metronidazole Linezolid	0.032-0.25 0.38-1.5		
	Tigecycline	0.064-1	0.25	0.75		Chloramphenicol	1–3		
D : (25)	D ' '''' C	0.016.0.125	0.016	0.047		Doxycycline	0.5-4		
Pa. micra (27)	Penicillin G Amoxicillin-clavulanic	0.016-0.125 0.016-0.75	0.016 0.032	0.047 0.094		Tigecycline	0.064-0.125		
	acid				Pt. lacrimalis (4)	Penicillin G	0.016-0.125		
	Cefotetan Cefoxitin	0.125-2 0.125-3	0.38 0.5	1.5 2		Amoxicillin-clavulanic acid	0.016-0.25		
	Ertapenem	0.123-3	0.3	0.125		Cefotetan	0.016-0.38		
	Meropenem	0.008-0.38	0.047	0.19		Cefoxitin	0.016-0.25		
	Levofloxacin	0.125-3	0.25	0.5		Ertapenem	0.002-0.012		
	Moxifloxacin Clindamycin	0.094–1.5 0.047–2	0.19 0.38	0.38 1.5		Meropenem Levofloxacin	0.002-0.016 3-8		
	Metronidazole	0.032 - > 256	0.094	0.25		Moxifloxacin	0.002-0.38		
	Linezolid	0.125-3	1	3		Clindamycin	0.016-0.38		
	Chloramphenicol Doxycycline	0.75–6 0.047–4	3 0.125	6 1		Metronidazole Linezolid	0.023-0.38 0.19-2		
	Tigecycline	0.016-0.38	0.123	0.125		Chloramphenicol	0.75-3		
D 1 1(15)		0.045.040		0.000		Doxycycline	0.125-4		
Pt. harei (16)	Penicillin G Amoxicillin-clavulanic	0.016-0.19 0.016-0.38	0.023 0.023	0.032 0.25		Tigecycline	0.023-0.25		
	acid			0.23	Pt. gorbachii (4)	Penicillin G	0.016-0.19		
	Cefotetan	0.38-8	0.5	1		Amoxicillin-clavulanic	0.016-0.064		
	Cefoxitin Ertapenem	0.023-1.5 0.006-0.023	0.094 0.012	0.5 0.016		acid Cefotetan	0.5-1.5		
	Meropenem	0.004-0.032	0.008	0.032		Cefoxitin	0.064-0.5		
	Levofloxacin	2–64	4	6		Ertapenem	0.012-0.023		
	Moxifloxacin Clindamycin	0.125-1.5 0.094-1.5	0.19 0.25	0.38 1.5		Meropenem Levofloxacin	0.004-0.064 3-64		
	Metronidazole	0.032-2	0.38	1.5		Moxifloxacin	0.19-0.5		
	Linezolid	0.5–2	0.75	1.5		Clindamycin	0.125-0.75		
	Chloramphenicol Doxycycline	1.5-4 0.064-24	3 8	3 16		Metronidazole Linezolid	0.023-0.5 0.75-1.5		
	Tigecycline	0.023-0.25	0.094	0.25		Chloramphenicol	2–3		
4 : 1: (0)	D 1.1111 C	0.016.0.004				Doxycycline	0.064-0.38		
A. vaginalis (8)	Penicillin G Amoxicillin-clavulanic	0.016-0.094 0.016-0.125				Tigecycline	0.016-0.094		
	acid				A. murdochii (3)	Penicillin G	0.016 – 0.75		
	Cefotetan Cefoxitin	0.094-0.5 0.032-0.125				Amoxicillin-clavulanic acid	0.032-0.25		
	Ertapenem	0.032-0.123				Cefotetan	0.75-8		
	Meropenem	0.006-0.125				Cefoxitin	0.125-1		
	Levofloxacin Moxifloxacin	24–64 0.5–2				Ertapenem Meropenem	0.19-2 0.125-0.75		
	Clindamycin	0.023 - > 256				Levofloxacin	1.5-4		
	Metronidazole	0.047-0.5				Moxifloxacin	0.25		
	Linezolid Chloramphenicol	0.38-1.5 1.5-3				Clindamycin Metronidazole	0.016-0.5 0.19-0.5		
	Doxycycline	0.125–16				Linezolid	0.19-0.5		
	Tigecycline	0.047-1.5				Chloramphenicol	1-3		
Dt inorii (5)	Donisillin C	0.016-0.047				Doxycycline Tigografina	0.25–16		
Pt. ivorii (5)	Penicillin G Amoxicillin-clavulanic	0.016-0.047				Tigecycline	0.047		
	acid				At. parvulum (4)	Penicillin G	0.094-0.25		
	Cefotetan Cefoxitin	0.125-1 0.125-0.75				Amoxicillin-clavulanic acid	0.064-0.25		
	Ertapenem	0.123-0.73				Cefotetan	2–8		
	Meropenem	0.002 - 0.016				Cefoxitin	1.5-3		
	Levofloxacin Moxifloxacin	0.38–64 0.094–64				Ertapenem Meropenem	0.032-0.19 0.125-0.25		
	Clindamycin	0.094-04				Levofloxacin	0.125-0.25		
	Metronidazole	0.094-0.25				Moxifloxacin	0.19 - 0.38		
	Linezolid	0.19-2				Clindamycin Metronidazole	1.5-6 0.19-0.5		
	Chloramphenicol	1–3							

Continued on following page

TABLE 2—Continued

Organism (no. of strains) a	Antibiotic	MIC (mg/liter)			Organism	Antibiotic	MIC (mg/liter)		
		Range	MIC ₅₀	MIC ₉₀	(no. of strains) ^a	Antibiotic	Range	MIC ₅₀	MIC ₉₀
	Chloramphenicol	4–16				Meropenem	0.125		
	Doxycycline	1-2				Levofloxacin	64		
	Tigecycline	0.064 - 0.5				Moxifloxacin	6		
	8.1,1					Clindamycin	0.38		
A. tetradius (2)	Penicillin G	0.023-0.032				Metronidazole	0.094		
	Amoxicillin-clavulanic	0.032-0.064				Linezolid	2		
	acid					Chloramphenicol	3		
	Cefotetan	0.25-0.5				Doxycycline	0.25		
	Cefoxitin	0.19-0.38				Tigecycline	0.094		
	Ertapenem	0.094-0.125				11800) 011110	0.05		
	Meropenem	0.094-0.125			A. lactolyticus (1)	Penicillin G	0.125		
	Levofloxacin	2–3			11. 111. 111. (1)	Amoxicillin-clavulanic	0.125		
	Moxifloxacin	0.19-0.38				acid	0.123		
	Clindamycin	1–4				Cefotetan	2		
	Metronidazole	0.25-0.75				Cefoxitin	0.5		
	Linezolid	1-1.5				Ertapenem	1		
	Chloramphenicol	3–3				Meropenem	0.38		
	Doxycycline	2–8				Levofloxacin	6		
	Tigecycline	0.125-0.19				Moxifloxacin	0.19		
	Tigecycline	0.123-0.19				Clindamycin	0.047		
Pt. octavius (1)	Penicillin G	0.125				Metronidazole	0.25		
1 i. Octavius (1)	Amoxicillin-clavulanic	0.064				Linezolid	0.38		
	acid	0.004				Chloramphenicol	1		
	Cefotetan	0.5				Doxycycline	0.38		
	Cefoxitin	0.25				Tigecycline	0.094		
	Ertapenem	0.094				Tigetycinie	0.054		
	Meropenem	0.094			GPAC (4)	Penicillin G	0.023-0.125		
	Levofloxacin	4			GFAC (4)	Amoxicillin-clavulanic	0.025-0.125		
	Moxifloxacin	0.5				acid	0.010-0.094		
	Clindamycin	0.047				Cefotetan	1–4		
	Metronidazole	0.047				Cefoxitin	0.125-1		
	Linezolid	0.38					0.125-1		
						Ertapenem			
	Chloramphenicol	2 0.19				Meropenem	0.008-0.75		
	Doxycycline					Levofloxacin	0.5-2		
	Tigecycline	0.064				Moxifloxacin	0.064-0.38		
R. gnavus (1)	D :: 'II' C	4			II	Clindamycin	0.094-0.125		
	Penicillin G	1			II	Metronidazole	0.064-0.38		
	Amoxicillin-clavulanic	0.19				Linezolid	0.5–1		
	acid	22			II	Chloramphenicol	1.5–3		
	Cefotetan	32				Doxycycline	0.094-1		
	Cefoxitin	4				Tigecycline	0.023 - 0.19		
	Ertapenem	0.38			11				

^a Genus abbreviations: Pe., Peptostreptococcus; Pa., Parvimonas; Pt., Peptoniphilus; A., Anaerococcus; R., Ruminococcus; At., Atopobium.

phenotypically distinguished from *Pt. asaccharolyticus* (10, 21). The combination of diminished antimicrobial susceptibility, its prevalence, and the described virulence factors (8) gives *F. magna* a special position among the GPAC.

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TABLE 3. Overall resistance of GPAC against 15 antibiotics^a

Antibiotic	MIC (mg/liter)					
Antibiotic	Range	MIC ₅₀	MIC ₉₀			
Penicillin G	0.016-2	0.047	0.19			
Amoxicillin-clavulanic acid	0.016-4	0.094	0.38			
Cefotetan	0.016 - 32	0.75	3			
Cefoxitin	0.016-4	0.5	2			
Ertapenem	0.002-2	0.064	0.19			
Meropenem	0.002-1	0.064	0.25			
Levofloxacin	0.094-64	0.75	64			
Moxifloxacin	0.002 - 64	0.25	1.5			
Clindamycin	0.016 -> 256	0.38	2			
Metronidazole	0.023 -> 256	0.19	0.75			
Linezolid	0.125-6	1.5	3			
Chloramphenicol	0.75-16	3	8			
Doxycycline	0.047-24	1	16			
Tigecycline	0.016-1.5	0.094	0.38			

 $^{^{\}it a}$ The overall resistance of GPAC (n=115) against various antibiotics is indicated.

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